Amendments to the Claims:

A list of the claims, including Claim 36 as currently amended, is set forth below.

1-35 (cancelled).

36. (Currently Amended) A method for hybridization of probes onto immobilized genomic DNA comprising the steps of:

(a) providing a sample containing or suspected of having genomic content, wherein said genomic content is undigested or intact chromosomal ~~genomic~~ DNA or RNA; ~~and~~

(b) denaturing said intact genomic content ~~DNA~~;

(c)~~(b)~~ immobilizing said denatured intact genomic content within ~~DNA onto~~ a matrix; said matrix comprising pore sizes within a range of 0.6 μm to 2 μm including the outer limits;

(d)~~(c)~~ providing a set of probes and passing said probes through said matrix under conditions favoring hybridization of the probes to its complementary sequence in said intact genomic content ~~DNA~~; and

(e)~~(d)~~ washing off non-hybridized probes through said matrix, leaving formed hybridized intact genomic content ~~DNA~~/probe complexes for further analysis.

37. (Previously Presented) The method according to claim 36, wherein said denatured intact genomic DNA is permeated within said matrix.

38. (Previously Presented) The method according to claim 36, wherein said probes are passed through said matrix by at least one cycle of alternating downwards and upwards flow.

39. (Previously Presented) The method according to claim 36, wherein said washing step is carried out by passing through said matrix a wash fluid by at least one cycle of downwards flow.

40. (Previously Presented) The method according to claim 36, wherein said matrix is a membrane.

41. (Previously Presented) The method according to claim 40, wherein said membrane comprises a 3D network structure.

42. (Previously Presented) The method according to claim 41, wherein said network structure is a flow-through structure.

43. (Previously Presented) The method according to claim 41, wherein said network structure is a fibre network structure.

44. (Previously Presented) The method according to claim 43, wherein said fibre is of vegetable origin.

45. (Previously Presented) The method according to claim 44, wherein said fibre is cellulose.

46. (Previously Presented) The method according to claim 36, wherein the matrix allows for a flow rate comprised between 50mm/30min and 250mm/30min including the outer limits.

47. (Previously Presented) The method according to claim 36, wherein said matrix is activated with an affinity conjugate.

48. (Previously Presented) The method according to claim 47, wherein said affinity conjugate is chosen from the group comprising poly-L-lysine, poly-D-lysine, 3- aminopropyl-triethoxysilane, poly-arginine, polyethyleneimine, polyvinylamine, polyallylamine, tetraethylenepentamine, ethylenediamine, diethylenetriamine, triethylenetetramine, pentaethylenehexamine and hexamethylenediamine.

49. (Previously Presented) The method according to claim 48, wherein said affinity conjugate is poly-L-lysine.

50. (Previously Presented) The method according to claim 36, wherein said probes are flanked by primer binding sequences.

51. (Previously Presented) A method for target nucleic acid detection and quantification in an intact genomic DNA sample comprising the steps of:

(a) providing intact genomic DNA and denaturing said intact genomic DNA;

(b) performing a hybridization according to the method of Claim 36;

(c) recovering hybridized probes; and essentially simultaneously amplifying any recovered probe using a single primer pair, each member of said primer pair binding

to each recovered probe onto the respective flanking primer binding sequences of said probe; and

(d) qualitatively and quantitatively analyzing the recovered amplified probes of step (c).

52. (Previously Presented) The method according to claim 51, wherein the analysis of step (d) is by microarray analysis.

53. (Previously Presented) The method according to claim 51, wherein each probe is flanked 5' and 3' by primer binding regions with said 5' and 3' flanking primer binding sequences being the same or substantially the same for each probe.

54. (Previously Presented) The method according to claim 51, wherein said amplification of step (c) is a quantitative amplification.

55. (Previously Presented) The method according to claim 54, wherein said amplification is by means of polymerase chain reaction.

56. (Previously Presented) The method according to claim 51, wherein the amplified probes are provided with a label.

57. (Previously Presented) The method according to claim 56, wherein said label is a fluorescent label.

58. (Previously Presented) A device for flow-through hybridization of probes onto immobilized intact genomic DNA comprising a well holder, said well holder comprising one or more round wells with a fixed diameter, said wells exposing a fibre network matrix, said matrix comprising pore sizes within a range of 0.6 μm to 2 μm including the outer limits; wherein said matrix permits immobilization of intact genomic DNA and which allows hybridization of said immobilized intact genomic material with probes by flow-through hybridization.

59. (Previously Presented) The device according to claim 58, wherein said matrix permits permeation of intact genomic DNA.

60. (Previously Presented) An apparatus for flow-through hybridization of probes onto immobilized genomic DNA comprising:

(a) a device according to claim 58;

(b) means for addition of a controlled amount of fluid to at least one of the wells of the device as described in (a);

(c) means for applying and/or maintaining a controlled pressure difference over the matrix in each of the wells.

61. (Previously Presented) A kit for flow-through hybridization of probes onto immobilized intact genomic DNA comprising:

(a) a device according to claim 58; and

(b) instructions.

62. (Previously Presented) A kit according to claim 61, additionally comprising:

(a) a set of probes, wherein each probe is flanked 5' end 3' by primer binding regions with said 5' and 3' flanking primer binding sequences being the same or substantially the same for each probe;

(b) a single primer pair, each member of said pair being complementary to a primer binding region;

(c) optionally amplification components allowing the amplification of any recovered hybridized probe; and

(d) optionally a microarray, said microarray allowing analysis of the hybridization results.